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NEW CLAIMS

1. Nucleic acid sequence, coding for a both tapetum-specific and pollen-specific promoter, the nucleic acid sequence comprising a range of at least 900 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1.
2. Nucleic acid sequence according to claim 1, characterized in that the nucleic acid sequence comprises a range of at least 1000 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1.
3. Nucleic acid sequence according to claim 1 or 2, characterized in that the nucleic acid sequence comprises a range of at least 1500 nucleotides upstream of the TATA box of the sequence represented in SEQ.ID. No. 1.
4. Nucleic acid sequence according to one of the claims 1 to 3, characterized in that the nucleic acid sequence comprises the sequence represented in SEQ.ID. No. 1.
5. Nucleic acid sequence coding for a both tapetum-specific and pollen-specific promoter, the nucleic acid sequence comprising the sequence represented in SEQ.ID. No. 2.
6. Nucleic acid sequence coding for a both tapetum-specific and pollen-specific promoter, the nucleic acid sequence comprising the sequence represented in SEQ.ID. No. 3.
7. Expression system, comprising at least one nucleic acid according to one of the claims 1 to 6.
8. Expression system according to claim 7, further comprising at least one terminator and/or a linker.
9. Nucleic acid construct, comprising a nucleic acid sequence according to one of the claims 1 to 6 and at least part of an expressible nucleic acid sequence selected from the group comprising expressible nucleic acid sequences, which code for translation products, which have a direct or indirect action and functional nucleic acids.
10. Nucleic acid construct according to claim 9, characterized in that the part of the expressible nucleic acid sequence or the complete expressible sequence is connected in the sense direction with the nucleic acid sequence according to one of the claims 1 to 6.
11. Nucleic acid sequence according to claim 9 or 10, characterized in that

the expressible nucleic acid codes for an invertase.

12. Nucleic acid construct according to claim 11, characterized in that the part of the nucleic acid sequence of an invertase or the complete sequence of an invertase is connected in the antisense direction with the nucleic acid sequence according to one of the claims 1 to 6.

13. Nucleic acid construct according to one of the claims 11 and 12, characterized in that the invertase is of the type present in a structure selected from the group comprising anthers, tapetum, pollen precursor cells and pollen.

14. Nucleic acid construct according to one of the claims 9 to 13, characterized in that the invertase comes from the organism or from the plant group including the species into which the nucleic acid construct is to be introduced.

15. Nucleic acid construct according to one of the claims 9 to 14, characterized in that the organism is selected from the group comprising food plants, ornamental plants and medicinal plants.

16. Vector comprising a nucleic acid sequence according to one of the claims 1 to 6 and/or an expression system according to one of the claims 7 and 8 and/or a nucleic acid construct according to one of the claims 9 to 15.

17. Cell, comprising a nucleic acid according to one of the claims 1 to 6 and/or an expression system according to one of the claims 7 and 8 and/or a nucleic acid construct according to one of the claims 9 to 15 and/or a vector according to claim 16.

18. Cell, characterized in that the cell comprises a nucleic acid sequence according to one of the claims 1 to 6, which is a promoter, and a nucleic acid coding for an inhibitor of an invertase, the promoter controlling the expression of the inhibitor.

19. Cell according to claim 17 or 18, characterized in that the cell is selected from the group comprising pollen cells, pollen precursor cells and tapetum cells.

20. Cell according to one of the claims 17 to 19, characterized in that the cell is an arrested pollen cell.

21. Plant comprising a cell according to one of the claims 17 to 20.

22. Plant according to claim 21, characterized in that the plant is selected

from the group comprising food plants, ornamental plants and medicinal plants and is preferably selected from the group comprising rice, maize, potatoes, tomatoes, rape, soya and sugar beet.

23. Plant according to claim 21 or 22, characterized in that the plant is a male, sterile plant and has at least one further modification of its genotype, particularly a modification caused by genetic engineering.

24. Seed of a plant according to one of the claims 21 to 23.

25. Hybrid seed, obtainable in that a male, sterile plant according to one of the claims 21 to 23 is hybridized with another male, fertile plant and the hybrid seed is obtained from the resulting filial generation.

26. Process for the production of male, sterile plants, characterized in that a nucleic acid construct according to one of the claims 11 to 15 is introduced into a cell, particularly into a plant cell and a plant is produced from said cell.

27. Process according to claim 26, characterized in that the plant is selected from the group comprising food plants, ornamental plants and medicinal plants and is preferably selected from the group comprising rice, maize, potatoes, tomatoes, rape, soya and sugar beet.

28. Use of a nucleic acid construct according to one of the claims 11 to 15, for producing sterile, male plants.

29. Use of a nucleic acid sequence according to one of the claims 1 to 6 for the expression of a nucleic acid sequence.

30. Restorer plant, characterized in that in a cell and preferably in most of its cells, it comprises a nucleic acid according to one of the claims 1 to 6 as promoter and a nucleic acid coding for a further invertase, which is controlled by said promoter, the further invertase differing from the cell's own invertase.

31. Restorer plant, preferably according to claim 30, characterized in that in a cell and preferably in most of its cells, it comprises a nucleic acid according to one of the claims 1 to 6 as promoter and a nucleic acid coding for a saccharose transport system and which is controlled by said promoter.

32. Restorer plant according to claim 31, characterized in that in a cell and preferably in most of its cells, it comprises a nucleic acid according to one of the claims 1 to 6 as promoter and a nucleic acid coding for saccharose synthase and/or cytoplasmically expressed invertase and whose expression is

controlled by the promoter.

33. Plant, characterized in that, in at least one cell and preferably in most of its cells, it comprises a nucleic acid construct according to one of the claims 11 to 15 and the cell or cells further comprise a nucleic acid sequence according to one of the claims 1 to 6 as promoter and a nucleic acid coding for a further invertase and which is controlled by said promoter, the further invertase differing from the cell's own invertase.

34. Plant, preferably according to claim 33, characterized in that in at least one cell and preferably in most of its cells, it comprises a nucleic acid construct according to one of the claims 11 to 15 and the cell or cells also comprise a nucleic acid sequence according to one of the claims 1 to 6 as promoter and a nucleic acid coding for a saccharose transport system, which is controlled by said promoter.

35. Plant, according to claim 34, characterized in that in at least one cell and preferably in most of its cells, it comprises a nucleic acid construct according to one of the claims 11 to 15 and the cell or cells also comprise a nucleic acid sequence according to one of the claims 1 to 6 as promoter and a nucleic acid coding for saccharose synthase and/or cytoplasmically expressed invertase, whose expression is controlled by the promoter.

36. Plant according to one of the claims 30 to 35, characterized in that the further invertase, differing from the cell's own invertase, is selected from the group of invertases comprising invertases of *Saccharomyces cerevisiae* and invertases of *Zymomonas mobilis*.

37. Plant according to one of the claims 31 to 36, characterized in that the saccharose synthase is of a heterologous or homologous origin.

38. Plant according to one of the claims 33 to 37, characterized in that the cytoplasmically expressed invertase is of a homologous or heterologous origin.

39. Plant according to claim 38, characterized in that the cytoplasmically expressed invertase is of a heterologous origin and is preferably selected from the group of invertases comprising invertases of *Saccharomyces cerevisiae* and invertases of *Zymomonas mobilis*.

40. Seed of a plant according to one of the claims 30 to 39.

41. Use of seed according to one of the preceding claims for the in vitro embryogenesis of haploid or diploid or double diploid plants.

42. Fruit, particularly seedless fruit, of a plant according to one of the claims 21 to 23.

43. Fruit of a plant according to one of the claims 30 to 39.

44. Process for cloning promoters, which are functionally homologous to one of the promoters according to one of the preceding claims, characterized by the following steps:

- c) cloning anther-specific invertase cDNA by RT-PCR of mRNA from anthers, particularly using oligonucleotides OIN3 and OIN4,
- d) cloning the corresponding promoters.